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RAW SEQUENCE LISTING

DATE: 01/24/2003

PATENT APPLICATION: US/10/080,522

TIME: 08:46:21

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\01242003\J080522.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

- 6 (i) APPLICANT: KAUFMAN, RUSSEL E.
7 SLENTZ-KESLER, KIMBERLY
9 (ii) TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER
10 CELLS
12 (iii) NUMBER OF SEQUENCES: 2
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
16 (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
17 (C) CITY: ARLINGTON
18 (D) STATE: VIRGINIA
19 (E) COUNTRY: U.S.A.
20 (F) ZIP: 22201-4714

22 (v) COMPUTER READABLE FORM:

- 23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

- C--> 29 (A) APPLICATION NUMBER: US/10/080,522
C--> 30 (B) FILING DATE: 25-Feb-2002
W--> 46 (C) CLASSIFICATION:

43 (vii) PRIOR APPLICATION DATA:

- 34 (A) APPLICATION NUMBER: US 09/539,774
35 (B) FILING DATE: 31-MAR-2000
39 (A) APPLICATION NUMBER: US 09/210,474
40 (B) FILING DATE: 14-DEC-1998
44 (A) APPLICATION NUMBER: US 08/755,559
45 (B) FILING DATE: 22-NOV-1996

48 (viii) ATTORNEY/AGENT INFORMATION:

- 49 (A) NAME: WILSON, MARY J.
50 (B) REGISTRATION NUMBER: 32,955
51 (C) REFERENCE/DOCKET NUMBER: 1579-645

53 (ix) TELECOMMUNICATION INFORMATION:

- 54 (A) TELEPHONE: (703) 816-4000
55 (B) TELEFAX: (703) 816-4100

58 (2) INFORMATION FOR SEQ ID NO: 1:

60 (i) SEQUENCE CHARACTERISTICS:

- 61 (A) LENGTH: 248 amino acids
62 (B) TYPE: amino acid
63 (C) STRANDEDNESS:
64 (D) TOPOLOGY: linear

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66 (ii) MOLECULE TYPE: protein
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73 Met Gln Thr Cys Pro Leu Ala Phe Pro Gly His Val Ser Gln Ala Leu
74 1 5 10 15
76 Gly Thr Leu Leu Phe Leu Ala Ala Ser Leu Ser Ala Gln Asn Glu Gly
77 20 25 30
79 Trp Asp Ser Pro Ile Cys Thr Glu Gly Val Val Ser Val Ser Trp Gly
80 35 40 45
82 Glu Asn Thr Val Met Ser Cys Asn Ile Ser Asn Ala Phe Ser His Val
83 50 55 60
85 Asn Ile Lys Leu Arg Ala His Gly Gln Glu Ser Ala Ile Phe Asn Glu
86 65 70 75 80
88 Val Ala Pro Gly Tyr Phe Ser Arg Asp Gly Trp Gln Leu Gln Val Gln
89 85 90 95
91 Gly Gly Val Ala Gln Leu Val Ile Lys Gly Ala Arg Asp Ser His Ala
92 100 105 110
94 Gly Leu Tyr Met Trp His Leu Val Gly His Gln Arg Asn Asn Arg Gln
95 115 120 125
97 Val Thr Leu Glu Val Ser Gly Ala Glu Pro Gln Ser Ala Pro Asp Thr
98 130 135 140
100 Gly Phe Trp Pro Val Pro Ala Val Val Thr Ala Val Phe Ile Leu Leu
101 145 150 155 160
103 Val Ala Leu Val Met Phe Ala Trp Tyr Arg Cys Arg Cys Ser Gln Gln
104 165 170 175
106 Arg Arg Glu Lys Lys Phe Phe Leu Leu Glu Pro Gln Met Lys Val Ala
107 180 185 190
109 Ala Leu Arg Ala Gly Ala Gln Gln Gly Leu Ser Arg Ala Ser Ala Glu
110 195 200 205
112 Leu Trp Thr Pro Asp Ser Glu Pro Thr Pro Arg Pro Leu Ala Leu Val
113 210 215 220
115 Phe Lys Pro Ser Pro Leu Gly Ala Leu Glu Leu Leu Ser Pro Gln Pro
116 225 230 235 240
118 Leu Phe Pro Tyr Ala Ala Asp Pro
119 245
126 (2) INFORMATION FOR SEQ ID NO: 2:
128 (i) SEQUENCE CHARACTERISTICS:
129 (A) LENGTH: 2180 base pairs
130 (B) TYPE: nucleic acid
131 (C) STRANDEDNESS: single
132 (D) TOPOLOGY: linear
134 (ii) MOLECULE TYPE: DNA (genomic)
139 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
141 ATTCCTGCTT CCTTTAGCGT GAACGCGGGT GCGGTGCCTC CCGTGAAATA ATAAATTCAC 60
143 CGTCACGCTT GTTGTGAACG CGGGTGGTTC CCGAAACTTG GAGGCTTCCC GTAAACCCAG 120
145 CTCCTTCCTC ATCTGGGAGG TGGGTCCCGC GCGGGTCCGC CGCTCCTCC CTGGCCCCCTC 180
147 CCTCTCGTGT CTTTCATTTT CCTGGGGCTC CGGGGCGCGG AGAAGCTGCA TCCCAGAGGA 240
149 GCGCGTCCAG GAGCGGACCC GGGAGTGTTC CAAGAGCCAG TGACAAGGAC CAGGGGCCCA 300
151 AGTCCCACCA GCCATGCAGA CTGCCCCCTT GGCATTCCCT GGCCACGTTT CCCAGGCCCT 360
153 TGGGACCCTC CTGTTTTTGG CTGCCTCCTT GAGTGCTCAG AATGAAGGCT GGGACAGCCC 420

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155	CATCTGCACA	GAGGGGGTAG	TCTCTGTGTC	TTGGGGCGAG	AACACCGTCA	TGTCCTGCAA	480
157	CATCTCCAAC	GCCTTCTCCC	ATGTCAACAT	CAAGCTGCGT	GCCCACGGGC	AGGAGAGCGC	540
159	CATCTTCAAT	GAGGTGGCTC	CAGGCTACTT	CTCCCGGGAC	GGCTGGCAGC	TCCAGGTTCA	600
161	GGGAGGCGTG	GCACAGCTGG	TGATCAAAGG	CGCCCGGGAC	TCCCATGCTG	GGCTGTACAT	660
163	GTGGCACCTC	GTGGGACACC	AGAGAAATAA	CAGACAAGTC	ACGCTGGAGG	TTTCAGGTGC	720
165	AGAACCCCAG	TCCGCCCTTG	ACACTGGGTT	CTGGCCTGTG	CCAGCGGTGG	TCACTGCTGT	780
167	CTTCATCCTC	TTGGTCGCTC	TGGTCATGTT	CGCCTGGTAC	AGGTGCCGCT	GTTCCCAGCA	840
169	ACGCCGGGAG	AAGAAGTTCT	TCCTCCTAGA	ACCCAGATG	AAGGTCGCAG	CCCTCAGAGC	900
171	GGGAGCCCAG	CAGGGCCTGA	GCAGAGCCTC	CGCTGAAC TG	TGGACCCCAG	ACTCCGAGCC	960
173	CACCCCAAGG	CCGCTGGCAC	TGGTGTTCAA	ACCCTCACCA	CTTGGAGCCC	TGGAGCTGCT	1020
175	GTCCCCCCCCA	ACCCTTGTTT	CCATATGCCG	CAGACCCATA	GCCGCCTGCA	AGGCAGAGAG	1080
177	GACACAGGAG	AGCCAGCCCT	GAGTGCCGAC	CTTGGGTGGC	GGGGCCTGGG	TCTCTCGTCC	1140
179	CACCCGGAGG	GCACAGACAC	CGGCTTGCTT	GGCAGGCTGG	GCCTCTGTGT	CACCCACTCC	1200
182	TGGGTGCGTG	CAGACCCCTC	CCCTCCACCC	CCCAGGTCTT	CCAAGCTCTG	CTTCCTCAGT	1260
184	TTCCAAAATG	GAACCACCTC	ACCTCCGCAG	CACCCGACTT	ACCAGGACGC	ATGCCCTCC	1320
186	CTCTGCCCTC	ATCAAACCCA	CAGACCCGGA	CTCCCTTTCT	GCCACCCCAG	GCTGGTCCGG	1380
188	CCCCAGGTGT	GGGGTCCGCT	CTCTCCACTC	CCAGGGCTCC	GCGCCCAAGT	GAGGGGGCCC	1440
190	CTGCCGGAGC	CTCAGACACA	CTGGAGTTCA	GGGCTGGGGG	GGCCTTGGCA	CATACCTGTC	1500
192	CCTTGGCTAT	GAGCAGGCTT	TGGGGGCCCT	TCCGCGGCAG	CCCCGGGGGC	CGAGGTAGGG	1560
194	TCTGGGGGCT	TAGAGGCTGG	GATGGCTCCT	GGCCCCACCG	CCAGGGGGCA	AGCGCAGGCC	1620
196	GGGCTGGGAG	GCGGCGGCGG	CGGCTCGGGC	TGGGGGGTCA	GGTGGACGCT	GCCTCCGGGG	1680
198	CTGGTCGCGC	ATCCCTCAGT	CCCTCGGCCA	CCCGGGGGTC	GCTCCCTCGT	GCCCACCGCA	1740
200	CCTGCCGAGC	CTCTTTGGAC	CCAGATCTGT	TCATGCTTTT	GTCTTCGTCA	CTGCGGCGGG	1800
202	GCCCTTTGAT	GTCTTCATCT	GTATGGGGTG	GAAAAATCAC	CGGGAATCCC	CCTTCAGTTC	1860
204	TTTGAAAAAG	TTCCATGACT	CGAATATCTG	AAATGAAGAA	AACAAACCGA	CTCACAAACC	1920
206	TCCAAGTAGC	TCCAAATGCA	ATTTTAAAAA	TGGAAAACAA	AAATCTGAAA	GAAACGTCTT	1980
208	TAGTGGCTTT	AAGCCCCAAA	ACGTCCCTAA	GGCGTCCTCG	AGATGAAGAC	GGGGGGGAGC	2040
210	CCCAGCCAGG	TGGAGACCCC	GCAGGACGCG	GCGGCGCCCG	GTGACCGAGG	CCTCGCACAG	2100
212	CCGCGCGCCC	TGAGGGTCTG	GCCGAGCCAG	GGTCCAAGAG	GGGCGCGTTT	GTGTCTCGGG	2160
214	TTAAATAAAG	GTTCCGTCCG					2180

VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:36 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:41 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:46 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)